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Thesis/Dissertation Sheet**Surname or Family name: **Yau**First name: **Sheree**

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Abbreviation for degree as given in the University calendar: **PhD**School: **Biotechnology and Biomolecular Sciences**Faculty: **Faculty of Science**Title: **Molecular microbial ecology of Antarctic lakes****Abstract 350 words maximum: (PLEASE TYPE)**

The Vestfold Hills is a coastal Antarctic oasis, a rare ice-free region on the continent containing hundreds of marine-derived lakes. These lakes are microbially-dominated systems constrained by extremes of cold, salinity and light availability. Most Antarctic lakes are ice-covered for a large proportion of the year and are thus largely closed systems that have often become meromictic (permanently stratified). The physical and chemical gradients that exist within a single isolated system makes it possible to relate microbial taxa to abiotic variables. These factors make Antarctic lakes ideal model ecosystems in which to study microbial diversity, evolution and influence on geochemistry.

Sequencing of ribosomal genes from the environment has revolutionised microbial ecology as it revealed the immense diversity of microbial life, however, this approach does not directly describe the physiology and ecological roles of members in a community. Random high-throughput sequencing of genetic material from the environment (metagenomics) allows the determination not only of the microbial community composition and structure, but also their metabolic potential. Metagenomic sequencing was applied to two meromictic lakes in the Vestfold Hills, Ace Lake and Organic Lake to in order to gain insight into the diversity and microbial processes occurring in different strata of the lakes. Analyses to support metagenomic inferences were also developed and applied. These included identification and quantification of proteins extracted directly from the environment (metaproteomics), which indicates active community members and biochemical processes, as well as microscopy for determination microbial/viral abundances and morphology.

Metagenomic sequencing revealed the abundance of virophages, a previously unknown viral family.

Taken in combination with both historic and contemporary physico-chemical data, molecular-based information allowed a description of the lake ecosystems and also resulted in new insights into mechanisms of adaptation to the Antarctic environment. From these genomic discoveries, hypotheses of the role previously unknown taxa and functional genes have on the environment were developed and modelled. These discoveries not only have implications for Antarctic environments, but also for other aquatic systems.

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